



PCT

RAW SEQUENCE LISTING

DATE: 07/16/2004

PATENT APPLICATION: US/10/501,039

TIME: 10:14:15

Input Set : A:\Sequence Listing PCT-JP03-00117.txt

Output Set: N:\CRF4\07162004\J501039.raw

3 <110> APPLICANT: Tetsuro Kokubo, Masahiro Shirakawa, and Jeremy Robin Howard Tame
 5 <120> TITLE OF INVENTION: Method of monitoring gene expression
 7 <130> FILE REFERENCE: 4439-4023
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/501,039
 C--> 10 <141> CURRENT FILING DATE: 2004-07-08
 12 <150> PRIOR APPLICATION NUMBER: JP P2002-002396
 13 <151> PRIOR FILING DATE: 2002-01-09
 15 <160> NUMBER OF SEQ ID NOS: 14
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2487
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Saccharomyces cerevisiae
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(2484)
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 31 1 5 10 15
 33 ggt tct tat att aat tat gag ggc ttg aaa aaa ttc ctg aag gaa gat 96
 34 Gly Ser Tyr Ile Asn Tyr Glu Gly Leu Lys Lys Phe Leu Lys Glu Asp
 35 20 25 30
 37 agc gtg aag gat gga agt aac gat aag aaa gca cgc tgg gac gat tca 144
 38 Ser Val Lys Asp Gly Ser Asn Asp Lys Lys Ala Arg Trp Asp Asp Ser
 39 35 40 45
 41 gat gaa tcc aag ttt gtg gaa gag ttg gat aag gaa ctt gaa aaa gtc 192
 42 Asp Glu Ser Lys Phe Val Glu Leu Asp Lys Glu Leu Glu Lys Val
 43 50 55 60
 45 tat ggt ttt caa cta aaa aag tac aat aac ttg atg gag aga ttg tcc 240
 46 Tyr Gly Phe Gln Leu Lys Lys Tyr Asn Asn Leu Met Glu Arg Leu Ser
 47 65 70 75 80
 49 cat ctg gag aaa caa aca gat acg gaa gca gcc ata aag gcc ttg gac 288
 50 His Leu Glu Lys Gln Thr Asp Thr Glu Ala Ala Ile Lys Ala Leu Asp
 51 85 90 95
 53 gct gat gca ttc caa cgt gta ttg gag gaa ctg tta agc gag tct acc 336
 54 Ala Asp Ala Phe Gln Arg Val Leu Glu Glu Leu Leu Ser Glu Ser Thr
 55 100 105 110
 57 gaa tta gac aat ttt aag aga ttg aac ttt act ggg ttt gct aag att 384
 58 Glu Leu Asp Asn Phe Lys Arg Leu Asn Phe Thr Gly Phe Ala Lys Ile
 59 115 120 125
 61 gtt aag aaa cat gac aag cta tat cca aag tat cca tct gtt aaa tct 432
 62 Val Lys Lys His Asp Lys Leu Tyr Pro Lys Tyr Pro Ser Val Lys Ser



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65 ttg ttg gaa gtt aga tta aag gaa ttg cct tcc cat tcg gaa gaa tat 480
66 Leu Leu Glu Val Arg Leu Lys Glu Leu Pro Ser His Ser Glu Glu Tyr
67 145      150      155      160
69 tcc cca ttg ttg tat cgt att tca ttt ttg tac aac att ttg aga agt 528
70 Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser
71      165      170      175
73 aat ttt aac act gca tct gaa ccc tta gcc agc gct tct aag ttt tct 576
74 Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser
75      180      185      190
77 agc att gtc agc aat gac ata gac atg aat ttc aga agc ttt aaa ttt 624
78 Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe
79      195      200      205
81 tgg gtt cat aat gac aac tta atg gag gtc aaa aca aga atc ttg aga 672
82 Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg
83      210      215      220
85 cat ctt ccc gtg ttg gtc tac gcc aat gtt ccc tcc gaa aac gat gac 720
86 His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp
87 225      230      235      240
89 ctg gtc aat aga ttc gaa tca gat ata tca aat aat gat gaa att gtg 768
90 Leu Val Asn Arg Phe Glu Ser Asp Ile Ser Asn Asn Asp Glu Ile Val
91      245      250      255
93 ggt agt tcg agc tcc act agt agc gta gaa cat ggc ttg gga gcg cgc 816
94 Gly Ser Ser Ser Ser Thr Ser Ser Val Glu His Gly Leu Gly Ala Arg
95      260      265      270
97 tcc ttc gat cca tta atc aac acg cta tat ttt gac aat gag cat ttt 864
98 Ser Phe Asp Pro Leu Ile Asn Thr Leu Tyr Phe Asp Asn Glu His Phe
99      275      280      285
101 gaa tta tat aac gac aag tta tta aag tta aat tca gca cct act tta 912
102 Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu
103      290      295      300
105 aga tta agg tgg act ggc cag tta tct gat aag ccg gat att ttc ttg 960
106 Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu
107 305      310      315      320
109 gaa aag aaa act ctt att gaa gac gaa gcc act ggg aag tct gaa ttt 1008
110 Glu Lys Lys Thr Leu Ile Glu Asp Glu Ala Thr Gly Lys Ser Glu Phe
111      325      330      335
113 gat cta act aaa ttg caa ttg aaa caa aaa ttc att aac ggg ttt att 1056
114 Asp Leu Thr Lys Leu Gln Leu Lys Gln Lys Phe Ile Asn Gly Phe Ile
115      340      345      350
117 ttc gaa ggt gat aag aaa ttt aaa gaa caa act ttg aaa aag tta aaa 1104
118 Phe Glu Gly Asp Lys Lys Phe Lys Glu Gln Thr Leu Lys Lys Leu Lys
119      355      360      365
121 gaa agt ggt acg gca ggg aga gac ctg gaa agg tta gaa gaa gat ttc 1152
122 Glu Ser Gly Thr Ala Gly Arg Asp Leu Glu Arg Leu Glu Glu Asp Phe
123      370      375      380
125 tct gag att caa aac ttt att atc aag aat gaa ttg caa cca gtt ttt 1200
126 Ser Glu Ile Gln Asn Phe Ile Ile Lys Asn Glu Leu Gln Pro Val Phe
127 385      390      395      400

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130 Arg Thr Val Tyr Thr Arg Thr Ala Phe Gln Ile Pro Gly Asp Asp Lys
131          405          410          415
133 ata aga gta acc att gac tct aat att gta ttc atc aag gag gat tca 1296
134 Ile Arg Val Thr Ile Asp Ser Asn Ile Val Phe Ile Lys Glu Asp Ser
135          420          425          430
137 ttc gac aga gag cgt cca att aga gac cct aat acc tgg cat aga act 1344
138 Phe Asp Arg Glu Arg Pro Ile Arg Asp Pro Asn Thr Trp His Arg Thr
139          435          440          445
141 gat att gat gcc aat gtt gca aat ccc ttg aaa ttc ctg aga gga ggc 1392
142 Asp Ile Asp Ala Asn Val Ala Asn Pro Leu Lys Phe Leu Arg Gly Gly
143          450          455          460
145 gag tat gct aag ttt cct tat tca gta atg gaa att aaa gtg aaa agt 1440
146 Glu Tyr Ala Lys Phe Pro Tyr Ser Val Met Glu Ile Lys Val Lys Ser
147 465          470          475          480
149 tca tta gat tct tcg atg tct gcc agt tct atg att tct aat gta aaa 1488
150 Ser Leu Asp Ser Ser Met Ser Ala Ser Ser Met Ile Ser Asn Val Lys
151          485          490          495
153 ctg cct aaa aag cat ggt caa tgg ctg aac gat ttg aca aat tct cat 1536
154 Leu Pro Lys Lys His Gly Gln Trp Leu Asn Asp Leu Thr Asn Ser His
155          500          505          510
157 ttg gtc aaa gaa att cca aag ttt tct atc ttt gtg caa ggt gtg gca 1584
158 Leu Val Lys Glu Ile Pro Lys Phe Ser Ile Phe Val Gln Gly Val Ala
159          515          520          525
161 tca ttg tat gga gat gat gaa aaa tta gat atc tta cca ttt tgg tta 1632
162 Ser Leu Tyr Gly Asp Asp Glu Lys Leu Asp Ile Leu Pro Phe Trp Leu
163          530          535          540
165 cca gat ttg gaa aca gat att aga cag gat cct aag caa gca tat gag 1680
166 Pro Asp Leu Glu Thr Asp Ile Arg Gln Asp Pro Lys Gln Ala Tyr Glu
167 545          550          555          560
169 gag gaa aag aaa aaa ctg ttg aaa caa aaa gag ata caa aag aaa att 1728
170 Glu Glu Lys Lys Lys Leu Leu Lys Gln Lys Glu Ile Gln Lys Lys Ile
171          565          570          575
173 gat gga atg aga agg ctt tcc aac tta aaa gag cct caa cat caa gca 1776
174 Asp Gly Met Arg Arg Leu Ser Asn Leu Lys Glu Pro Gln His Gln Ala
175          580          585          590
177 gca gta ccg gta tct caa gag gaa aat gag cgt att acc tct caa ggt 1824
178 Ala Val Pro Val Ser Gln Glu Glu Asn Glu Arg Ile Thr Ser Gln Gly
179          595          600          605
181 gat ttg gag gca gac ggt tca tcc gat gag gaa act gag caa gaa cct 1872
182 Asp Leu Glu Ala Asp Gly Ser Ser Asp Glu Glu Thr Glu Gln Glu Pro
183          610          615          620
185 cat tcg aaa aga tca aag aaa gtt cgg aga aga aaa ccc aag gcc act 1920
186 His Ser Lys Arg Ser Lys Lys Val Arg Arg Arg Lys Pro Lys Ala Thr
187 625          630          635          640
189 ttc ttg aga att ttg gcc ggt aga gat cca aag tta atg ggg gtg gat 1968
190 Phe Leu Arg Ile Leu Ala Gly Arg Asp Pro Lys Leu Met Gly Val Asp
191          645          650          655
193 tct gaa gaa gaa gaa att gaa ttg cca cct ggt gtg aaa aaa cca tta 2016

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194 Ser Glu Glu Glu Glu Ile Glu Leu Pro Pro Gly Val Lys Lys Pro Leu
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198 Asn Leu Leu Lys Asn Ala Gly Pro Val Asn Val Glu Ala Lys Val Trp
199          675          680          685
201 ctt gcc aac gaa cgt aca ttt aac aga tgg tta agt gtc acc agt tta 2112
202 Leu Ala Asn Glu Arg Thr Phe Asn Arg Trp Leu Ser Val Thr Ser Leu
203          690          695          700
205 ttg agt gtt ttg acg ttc tca att tat aat tct gtg aag aaa gcc gaa 2160
206 Leu Ser Val Leu Thr Phe Ser Ile Tyr Asn Ser Val Lys Lys Ala Glu
207 705          710          715          720
209 tac ccc act ttg gct aac tac atg gca tac gta tat ttt ggt cta acg 2208
210 Tyr Pro Thr Leu Ala Asn Tyr Met Ala Tyr Val Tyr Phe Gly Leu Thr
211          725          730          735
213 ata ttc tgt gct tta tgg tcc tat tcc att tat atg aaa aga gtt gat 2256
214 Ile Phe Cys Ala Leu Trp Ser Tyr Ser Ile Tyr Met Lys Arg Val Asp
215          740          745          750
217 att att caa caa aga agc ggt caa cat cta gat gca cca ctt ggt cca 2304
218 Ile Ile Gln Gln Arg Ser Gly Gln His Leu Asp Ala Pro Leu Gly Pro
219          755          760          765
221 gtt ttg gtt tct ata gtt tta ttt gtc act tta gtg gtt aat ttt gtt 2352
222 Val Leu Val Ser Ile Val Leu Phe Val Thr Leu Val Val Asn Phe Val
223          770          775          780
225 atg gcg ttt aga aat gca gca aag tct cgt caa gag ttg caa ata cag 2400
226 Met Ala Phe Arg Asn Ala Ala Lys Ser Arg Gln Glu Leu Gln Ile Gln
227 785          790          795          800
229 aat tta gaa gtt cct gaa aga ata cca gaa gta tta agg cca ctt caa 2448
230 Asn Leu Glu Val Pro Glu Arg Ile Pro Glu Val Leu Arg Pro Leu Gln
231          805          810          815
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248          20          25          30
250 Ser Val Lys Asp Gly Ser Asn Asp Lys Lys Ala Arg Trp Asp Asp Ser
251          35          40          45
253 Asp Glu Ser Lys Phe Val Glu Glu Leu Asp Lys Glu Leu Glu Lys Val
254          50          55          60
256 Tyr Gly Phe Gln Leu Lys Lys Tyr Asn Asn Leu Met Glu Arg Leu Ser
257 65          70          75          80
259 His Leu Glu Lys Gln Thr Asp Thr Glu Ala Ala Ile Lys Ala Leu Asp
260          85          90          95

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262 Ala Asp Ala Phe Gln Arg Val Leu Glu Glu Leu Leu Ser Glu Ser Thr
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266          115          120          125
268 Val Lys Lys His Asp Lys Leu Tyr Pro Lys Tyr Pro Ser Val Lys Ser
269          130          135          140
271 Leu Leu Glu Val Arg Leu Lys Glu Leu Pro Ser His Ser Glu Glu Tyr
272 145          150          155          160
274 Ser Pro Leu Leu Tyr Arg Ile Ser Phe Leu Tyr Asn Ile Leu Arg Ser
275          165          170          175
277 Asn Phe Asn Thr Ala Ser Glu Pro Leu Ala Ser Ala Ser Lys Phe Ser
278          180          185          190
280 Ser Ile Val Ser Asn Asp Ile Asp Met Asn Phe Arg Ser Phe Lys Phe
281          195          200          205
283 Trp Val His Asn Asp Asn Leu Met Glu Val Lys Thr Arg Ile Leu Arg
284          210          215          220
286 His Leu Pro Val Leu Val Tyr Ala Asn Val Pro Ser Glu Asn Asp Asp
287 225          230          235          240
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290          245          250          255
292 Gly Ser Ser Ser Ser Thr Ser Ser Val Glu His Gly Leu Gly Ala Arg
293          260          265          270
295 Ser Phe Asp Pro Leu Ile Asn Thr Leu Tyr Phe Asp Asn Glu His Phe
296          275          280          285
298 Glu Leu Tyr Asn Asp Lys Leu Leu Lys Leu Asn Ser Ala Pro Thr Leu
299          290          295          300
301 Arg Leu Arg Trp Thr Gly Gln Leu Ser Asp Lys Pro Asp Ile Phe Leu
302 305          310          315          320
304 Glu Lys Lys Thr Leu Ile Glu Asp Glu Ala Thr Gly Lys Ser Glu Phe
305          325          330          335
307 Asp Leu Thr Lys Leu Gln Leu Lys Gln Lys Phe Ile Asn Gly Phe Ile
308          340          345          350
310 Phe Glu Gly Asp Lys Lys Phe Lys Glu Gln Thr Leu Lys Lys Leu Lys
311          355          360          365
313 Glu Ser Gly Thr Ala Gly Arg Asp Leu Glu Arg Leu Glu Glu Asp Phe
314          370          375          380
316 Ser Glu Ile Gln Asn Phe Ile Ile Lys Asn Glu Leu Gln Pro Val Phe
317 385          390          395          400
319 Arg Thr Val Tyr Thr Arg Thr Ala Phe Gln Ile Pro Gly Asp Asp Lys
320          405          410          415
322 Ile Arg Val Thr Ile Asp Ser Asn Ile Val Phe Ile Lys Glu Asp Ser
323          420          425          430
325 Phe Asp Arg Glu Arg Pro Ile Arg Asp Pro Asn Thr Trp His Arg Thr
326          435          440          445
328 Asp Ile Asp Ala Asn Val Ala Asn Pro Leu Lys Phe Leu Arg Gly Gly
329          450          455          460
331 Glu Tyr Ala Lys Phe Pro Tyr Ser Val Met Glu Ile Lys Val Lys Ser
332 465          470          475          480
334 Ser Leu Asp Ser Ser Met Ser Ala Ser Ser Met Ile Ser Asn Val Lys

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date